Amendments to the Specification :

Please amend the specification as follows:

Replace the paragraph beginning at page 66, line 7 and continuing to page 67, line 5, with the following re-written paragraph:

--The oviduct was removed from a Japanese quail (*Coturnix coturnix japonica*) and the magnum portion minced and enzymatically dissociated with 0.8 mg/ml collagenase (Sigma Chemical Co., St. Louis, MO) and 1.0 mg/ml dispase (Roche Molecular Biochemicals, Indianapolis, IN) by shaking and titurating for 30 minutes at 37°C. The cell suspension was then filtered through sterile surgical gauze, washed three times with F-12 medium (Life Technologies, Grand Island, NY) by centrifugation at 200 x *g*, and resuspended in OPTIMEM™ (Life Technologies) such that the OD_{600} was approximately 2. Cell suspension (300 µl) was plated per well of a 24-well dish. For each transfection, 2.5 µl of DMRIE-C liposomes (Life Technologies) and 1 µg of DNA were preincubated for 15 minutes at room temperature in 100 µl of OPTIMEM™, and then added to the oviduct cells. Cells with DNA/liposomes were incubated for 5 hours at 37°C in 5% CO_2. Next, 0.75 ml of DMEM (Life Technologies) supplemented with 15% fetal bovine serum (FBS) (Atlanta Biologicals, Atlanta, GA), 2X penicillin/streptomycin (Life Technologies), 10^{-6} M insulin (Sigma), 10^{-8} M ~~β-estradiol~~ ß-estradiol (Sigma), and 10^{-7} M corticosterone (Sigma) was added to each well, and incubation was continued for 72 hours. Medium was then harvested and centrifuged at 110 x *g* for 5 minutes. The supernatant was analyzed by ELISA for human interferon α2b content.--

Replace the paragraph beginning at page 37, line 1, with the following re-written paragraph:

--One aspect of the present invention, therefore, provides a novel isolated nucleic acid that comprises the nucleotide sequence SEQ ID NO: 67, shown in Fig. 5 (Genbank Accession No. AF405540) and derivatives and variants thereof, that is located immediately

5' upstream of the native lysozyme-encoding region of the chicken lysozyme gene locus.--

Replace the paragraph beginning at page 25, line 12 and continuing to page 26, line 9, with the following re-written paragraph:

--The terms "percent sequence identity" or "percent sequence similarity" as used herein refer to the degree of sequence identity between two nucleic acid sequences or two amino acid sequences as determined using the algorithm of Karlin and Attschul, 1990, *Proc. Natl. Acad. Sci.* 87: 2264-2268, modified as in Karlin and Attschul, 1993, *Proc. Natl. Acad. Sci.* 90: 5873-5877. Such an algorithm is incorporated into the NBLAST and XBLAST programs of Attschul *et al.*, 1990, *T. Mol. Biol.* Q15: 403-410. BLAST nucleotide searches are performed with the NBLAST program, score = 100, wordlength = 12, to obtain nucleotide sequences homologous to a nucleic acid molecule of the invention. BLAST protein searches are performed with the XBLAST program, score = 50, wordlength = 3, to obtain amino acid sequences homologous to a reference polypeptide. To obtain gapped alignments for comparison purposes, Gapped BLAST is utilized as described in Attschul *et al.*, 1997, *Nucl. Acids Res.* 25: 3389-3402. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g. XBLAST and NBLAST) are used. See www.ncbi.nlm.nih.gov ~~http://www.ncbi.nlm.nih.gov~~. Other algorithms, programs and default settings may also be suitable such as, but not only, the GCG-Sequence Analysis Package of the U.K. Human Genome Mapping Project Resource Centre that includes programs for nucleotide or amino acid sequence comparisons.--

Replace the Abstract at page 80, with the following re-written abstract:

--The invention includes isolated gene expression controlling regions which can be useful for expression of operably linked heterologous nucleic acids in cells such as oviduct cells.--